

Appl. No. 09/877,933  
AMENDMENT FAXED ON JANUARY 20, 2005  
REPLY TO OFFICE ACTION OF DECEMBER 2, 2004

PATENT

### REMARKS/ARGUMENTS

Claims 1-6 and 8-16 are presently under consideration and stand substantively rejected. Claims 7 and 17-31 were previously canceled. This response amends claims 1 and 14, cancels claim 4, and adds new claims 32 and 33. Support for the amendment to claims 1 and 14 can be found throughout the specification and at least at page 17, line 24 to page 21, line 5. Support for new claims 32 and 33 can be found throughout the specification and at least at page 5, lines 24-25. Reconsideration of the claims is respectfully requested. The paragraph numbering below follows that of the Office Action.

#### ¶3. Rejection Under 35 U.S.C. §112

Claims 1-16 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking written description in that the application allegedly provides written description only for capture reagents comprising antibodies.

For the purposes of expediting prosecution independent claims 1 and 14 have been amended to recite capture reagents comprising an antibody. Claims 2, 3, 5, 6, and 8-13, and claims 15 and 16 depend either directly or indirectly from independent amended claims 1 and 14, respectively and satisfy the written description requirement for the same reasons. Therefore, the written description requirement should be withdrawn.

Applicants note for the record their disagreement with the Examiner's position. According to MPEP 2163.02, to satisfy the written description requirement, an applicant must convey with reasonable clarity to the artisan that the inventor had possession, as of the filing date sought, of the subject matter now claimed. Applicants respectfully submit that the specification at p. 17, lines 25-29 provides written description of capture reagents encompassing any molecule that is capable of specifically binding to PDI meet the written description requirements.

#### ¶4. Rejection Under 35 U.S.C. §102

Claims 14 and 15 were rejected under 35 U.S.C. §102(e) as allegedly anticipated by U.S. Patent No. 5,798,249 to Braxton et al. ["Braxton"]. This rejection is traversed as follows.

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MPEP 2131 establishes that to anticipate a claim, a cited reference must teach every element of the claim.

According to the Action, Braxton describes a novel *human* protein disulfide isomerase (PDI). Yet amended claim 14 recites a protein disulfide isomerase of *Cryptosporidium parvum*, which is not the same as the human PDI described by Braxton. The attached BLAST report shows little sequence identity between the two. Applicants submit that Braxton fails to teach or suggest an antibody which binds to a protein disulfide isomerase of *Cryptosporidium parvum* as presently claimed, and therefore Braxton fails to anticipate amended claim 14.

Claim 15 depends from claim 14, and is therefore allowable as depending from an allowable base claim, as well as for the novel combination of elements it recites. Withdrawal of this rejection is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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NSC:nep  
Attachment: BLAST report and sequences  
60377226 v1

BEST AVAILABLE COPY

NCBI BLAST 2 sequences BLAST Entrez ?

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.2 [Dec-14-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
x\_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Sequence 1 lcl|seq\_1 Length 405 (1..405)  
Sequence 2 lcl|seq\_2 Length 481 (1..481)

Protein Disulfide Isomerase (PDI)

Human  
vs.  
*C. parvum*



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 79.0 bits (193), Expect = 6e-14  
Identities = 85/351 (24%), Positives = 148/351 (41%), Gaps = 33/351 (9%)

Query: 27 VTTEITSLATENIDEILNNADVALVNFYADWCRFSQMLHPIFEEASDVKEEFPNENQVV 86  
++ ITSL + N ++ + + + +V F+A WC L P F+ I + P V  
Sbjct: 31 ISEHITSLTSSNFEDFIKSKEHVIVTFAPWCGHCTALEPEFKATCAEISKLSLSP---PVH 87

Query: 87 FARVDCDQHSIDIAQRYRISKYPTLKLFRNGMMMKREYRGQSVKALADYIROQKSDPIQE 146  
VD ++ ++AQ+Y +S YPT+K F +G+ + Y G RS A YI++ +Q  
Sbjct: 88 CGSVDATENMELAQYGVSGYPTIKFP-SCIDSVQNVSGARSKDAFIKYIKLTKGPAVQV 146

Query: 147 IRDLAEITTLDRSKRN-IIG-YEQKSDNYRVFERNVILHD-DCAFLSAF--GDVSKPE 201  
I T+ S + +G+ XDS Y VFE+VA+ + + AF++ F G+  
Sbjct: 147 AESEEAIKTIFASSSSAFVGRFTSKDSABYAVFEKVASGHREHNYAFIAFFQGEQKLEV 206

Query: 202 RYSGDNIIYKPPGHSAPDMVYLGMATNFVDVTYNWIQDKCVPLVREITFEN-GEELTEHGL 260  
+ + + P + ++ ++ N VFL I+ EN ++ EG  
Sbjct: 207 LHKDEEPVSLPMPKTVEELEAKISIMN-----VPLFSAISAENYSLYMSREGY 254

Query: 261 PFLILFHKEDTESLEIFONEVARQLISEKGTINFLHADCDKF-RHPLLH--IQKTPA-D 316  
E + + + + + F+ D ++F H H I+K P  
Sbjct: 255 TANFC---GTNEDEFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQHLLIEKFPGLV 310

Query: 317 CPVLAIDSFREMYVFGDFKDVLIPIGKLKQFVFDLHSGKLHREFPHHGPDPTD 367  
+ + S R+MY F V LK+F+ + GK P P +  
Sbjct: 311 IQSVNVPSIRYMYGPAKFDSV---EPLKEFMKQVSEGGHLSIKSEPIPAE 358

Score = 52.8 bits (125), Expect = 5e-06  
Identities = 32/121 (26%), Positives = 63/121 (51%), Gaps = 6/121 (4%)

Query: 31 ITSLATENIDEILNNADV-ALVNFYADWCRFSQMLHPIFEEASDVKEEFPNENQVV 89  
+T + + +EI+ +D L+ YA WC + L PI+ + + EE+ + ++VV A+  
Sbjct: 363 VTVVVGKTFEEIVFRSDKDVLLIYAQWCGHCKNLEPIYNQ----LGEEYKDNKVVIAK 418

Query: 90 VDCDQHSDIAQRYRISKYPTLKLFRNGMMKREYRGQRSEVKALADYIRQQKSDPIQ-BIR 148  
++ Q+ + + +PT+ + G Y G+R+V+A ++I + S P + E R  
Sbjct: 419 INGPQNDIPYEGFSPPRAEFTILFVKAGTRTPIPYDGKRTVRAFKETISEHSSFFQEKESR 478

Query: 149 D 149

D

Sbjct: 479 D 479

CPU time: 0.05 user secs. 0.00 sys. secs 0.05 total secs.

Gapped

Lambda	K	H
0.321	0.138	0.414

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1380

Number of Sequences: 0

Number of extensions: 121

Number of successful extensions: 6

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 405

length of database: 181,542,687

effective HSP length: 120

effective length of query: 285

effective length of database: 127,752,327

effective search space: 36409413195

effective search space used: 36409413195

T: 9

A: 40

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 71 (32.0 bits)

SEQ ID NO:2 of US Pat. No. 5,798,249 to Braxton et al. (USSN 08/650,275)  
Deduced Amino Acid Sequence of Human Protein Disulfide Isomerase (PDI)

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu  
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr  
Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn Ala Asp Val  
Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe Ser Gln Met Leu  
His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile Lys Glu Glu Phe Pro  
Asn Glu Asn Gln Val Val Phe Ala Arg Val Asp Cys Asp Gln His Ser  
Asp Ile Ala Gln Arg Tyr Arg Ile Ser Lys Tyr Pro Thr Leu Lys Leu  
Phe Arg Asn Gly Met Met Met Lys Arg Glu Tyr Arg Gly Gln Arg Ser  
Val Lys Ala Leu Ala Asp Tyr Ile Arg Gln Gln Lys Ser Asp Pro Ile  
Gln Glu Ile Arg Asp Leu Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys  
Arg Asn Ile Ile Gly Tyr Xaa Glu Gln Lys Asp Ser Asp Asn Tyr Arg  
Val Phe Glu Arg Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu  
Ser Ala Phe Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn  
Ile Ile Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu  
Gly Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu Leu  
Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys Glu Asp  
Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg Gln Leu Ile  
Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp Cys Asp Lys Phe  
Arg His Pro Leu Leu His Ile Gln Lys Thr Pro Ala Asp Cys Pro Val  
Ile Ala Ile Asp Ser Phe Arg His Met Tyr Val Phe Gly Asp Phe Lys  
Asp Val Leu Ile Pro Gly Lys Leu Lys Gln Phe Val Phe Asp Leu His  
Ser Gly Lys Leu His Arg Glu Phe His His Gly Pro Asp Pro Thr Asp  
Thr Ala Pro Gly Glu Gln Ala Gln Asp Val Ala Ser Ser Pro Pro Glu  
Ser Ser Phe Gln Lys Leu Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu  
Arg Asp Arg Asp Glu Leu

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTTETSLATENIDEILNNADVALVNFYADWCRF  
SQMLHPFEEASDVKEEFPNENQVVFARVDCDQHSDLAQRYSKYPTLKLFRNGMMM  
KREYRGQRSVKALADYIRQKSDPIQIBIRDLAETITLDRSKRNIIGYEQKDSNDYRVFER  
VANILHDDCAFLSAFGDVSKPERYSGDNIYKPPGHSAPDMVYLGAMTNFEDVTYNWIQ  
DKCVPLVREITFENGEBLTREGLPFLILPHMKEDTESLIFQNEVARQLISEKGTINFLHAD  
CDKFRHPLLIHQKTPADCPVIAIDSRHMYVFGDFKDVLPGLKQFVFDLHSGKLHREF  
HHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

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SEQ ID NO:2 of Instant Application (USSN 09/877,933)

Attorney Docket No. 014907-001910US

Deduced Amino Acid Sequences of *C. parvum* Protein Disulfide Isomerase (PDI)

Met Ile Gly Ile Arg Ser Leu Val Ser Ala Ala Phe Leu Gly Phe Ser  
Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser  
Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys  
Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His  
Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser  
Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn  
Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys  
Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser  
Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val  
Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser  
Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr  
Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala  
Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His  
Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu  
Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile  
Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala  
Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile  
Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu  
Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu  
Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg  
Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu  
Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser  
Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly  
Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu  
Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile  
Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile  
Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser  
Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr  
Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe  
Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu  
Leu

MIGIRSLVSA AFLGFSCLSKVVLGGDBAHFISEHTSLTSSNFEDFIKSKEHVIVTFFAPWC  
GHCTALEPEFKATCA BISKLSPPVHCGSV DATENMELAQQYGVSGYPTIKFFSGIDSVQN  
YSGARSKDAFIKYIKKLTGPAVQVAESEBAIKTIFASSSSAFVGRFTSKDSA EYAVFEKVA  
SGHREHNYAFLAFFQEGEQKLEVLHKDEEPVSLPMPKTVERLEAKISIMNVPLFSAISAEN  
YSLYMSREGYTA WFCGTNEDFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQHLL  
IEKFPGLVIQSVNVPSIRYMYGPAKFDSVEPLKEFMKQVSEGKHBLSIKSEPIPAEQSGPV  
TVVVGKTFEEIVFRSDKDVLL EY AQWCGHCKNLEPIYNQLGEEYKDNDKVVIKINGP  
QNDIPYEGFSFRAFPTILFVKAGTRTPIPYDGKRTVEAFKEFISEHSSFPQEKESRDEL

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